

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Takaaki Sato and Junn Yanagisawa
- (ii) TITLE OF INVENTION: COMPOUNDS THAT INHIBIT THE  
INTERACTION BETWEEN SIGNAL-TRANSDUCING  
PROTEINS AND THE GLGF (PDZ/DHR) DOMAIN AND  
USES THEREOF
- (iii) NUMBER OF SEQUENCES: 33
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Cooper & Dunham LLP
  - (B) STREET: 1185 Avenue of the Americas
  - (C) CITY: New York
  - (D) STATE: New York
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: Not Yet Known
  - (B) FILING DATE: 18-JUL-1997
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: White, John P
  - (B) REGISTRATION NUMBER: 28,678
  - (C) REFERENCE/DOCKET NUMBER: 0575/48962-A-PCT-US
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (212) 278-0400
  - (B) TELEFAX: (212) 391-0525

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1
  - (D) OTHER INFORMATION: /product= "OTHER"/note= "Xaa= Gly/Ser/Ala/Glu"
- (ix) FEATURE:
  - (A) NAME/KEY: Protein
  - (B) LOCATION: 4
  - (D) OTHER INFORMATION: /product= "OTHER"/note= "Xaa= Phe/Ile/Leu"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Xaa Leu Gly Xaa  
1

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 6 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

    (A) NAME/KEY: Peptide  
    (B) LOCATION: 1  
    (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa=Lys/Arg/Gln"

(ix) FEATURE:

    (A) NAME/KEY: Peptide  
    (B) LOCATION: 2  
    (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa= Gly/Ser/Ala/Glu"

(ix) FEATURE:

    (A) NAME/KEY: Peptide  
    (B) LOCATION: 5  
    (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa= Phe/Ile/Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa Xaa Xaa Leu Gly Xaa  
1                    5

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 4 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ser Leu Gly Ile  
1

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 3 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
    (A) NAME/KEY: Peptide  
    (B) LOCATION: 1  
    (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa= Ser/Thr"

(ix) FEATURE:  
    (A) NAME/KEY: Peptide  
    (B) LOCATION: 3  
    (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa= Val/Ile/Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Xaa Xaa Xaa  
1

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val  
1                    5                    10                    15

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Ile Ser Asn Ser Arg Asn Glu Asn Glu Gly Gln Ser Leu Glu  
1                    5                    10                    15

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 15 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ser Thr Pro Asp Thr Gly Asn Glu Asn Glu Gly Gln Cys Leu Glu  
1                    5                    10                    15

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Glu Ser Leu Val  
1

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Thr Ile Gln Ser Val Ile  
1 5

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Arg Gly Phe Ile Ser Ser Leu Val  
1 5

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Arg Glu Thr Ile Glu Ser Thr Val  
1 5

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gln	Asn	Phe	Arg	Thr	Tyr	Ile	Val	Ser	Phe	Val
1				5					10	

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ser	Asp	Ser	Asn	Met	Asn	Met	Asn	Glu	Leu	Ser	Glu	Val
1				5					10			

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Pro	Pro	Thr	Cys	Ser	Gln	Ala	Asn	Ser	Gly	Arg	Ile	Ser	Thr	Leu
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ile	Asp	Leu	Ala	Ser	Glu	Phe	Leu	Phe	Leu	Ser	Asn	Ser	Phe	Leu
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Asp	Ser	Glu	Met	Tyr	Asn	Phe	Arg	Ser	Gln	Leu	Ala	Ser	Val	Val
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ile	Pro	Pro	Asp	Ser	Glu	Asp	Gly	Asn	Glu	Glu	Gln	Ser	Leu	Val
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gln	Ser	Leu	Val
1			

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ile	Gln	Ser	Leu	Val
1			5	

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Glu	Ile	Gln	Ser	Leu	Val
-----	-----	-----	-----	-----	-----

5

(2) INFORMATION FOR SEQ ID NO:21:

- (xi) SEQUENCE DESCRIPTION: SEO ID NO:21:

Asn Glu Ile Gln Ser Leu Val  
1 5

(2) INFORMATION FOR SEO ID NO:22:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Arg Asn Glu Ile Gln Ser Leu Val  
1 5

(2) INFORMATION FOR SEQ ID NO:23:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:24:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu  
1 5 10 15

Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys  
20 25 30

Pro	Thr	Gly 35	Leu	Tyr	Thr	His	Ser 40	Gly	Glu	Cys	Cys	Lys 45	Ala	Cys	Asn
Leu	Gly 50	Glu	Gly	Val	Ala	Gln 55	Pro	Cys	Gly	Ala	Asn 60	Gln	Thr	Val	Cys
Glu 65	Pro	Cys	Leu	Asp	Ser 70	Val	Thr	Phe	Ser	Asp 75	Val	Val	Ser	Ala	Thr 80
Glu	Pro	Cys	Lys	Pro 85	Cys	Thr	Glu	Cys	Val 90	Gly	Leu	Gln	Ser	Met 95	Ser
Ala	Pro	Cys	Val 100	Glu	Ala	Asp	Asp	Ala 105	Val	Cys	Arg	Cys	Ala 110	Tyr	Gly
Tyr	Tyr	Gln 115	Asp	Glu	Thr	Thr	Gly 120	Arg	Cys	Glu	Ala	Cys 125	Arg	Val	Cys
Glu	Ala 130	Gly	Ser	Gly	Leu	Val 135	Phe	Ser	Cys	Gln	Asp 140	Lys	Gln	Asn	Thr
Val 145	Cys	Glu	Glu	Cys	Pro 150	Asp	Gly	Thr	Tyr	Ser 155	Asp	Glu	Ala	Asn	His 160
Val	Asp	Pro	Cys	Leu 165	Pro	Cys	Thr	Val	Cys 170	Glu	Asp	Thr	Glu	Arg 175	Gln
Leu	Arg	Glu	Cys 180	Thr	Arg	Trp	Ala	Asp 185	Ala	Glu	Cys	Glu	Glu 190	Ile	Pro
Gly	Arg	Trp 195	Ile	Thr	Arg	Ser	Thr 200	Pro	Pro	Glu	Gly	Ser 205	Asp	Ser	Thr
Ala	Pro 210	Ser	Thr	Gln	Glu	Pro 215	Glu	Ala	Pro	Pro	Glu 220	Gln	Asp	Leu	Ile
Ala 225	Ser	Thr	Val	Ala	Gly 230	Val	Val	Thr	Thr	Val 235	Met	Gly	Ser	Ser	Gln 240
Pro	Val	Val	Thr	Arg 245	Gly	Thr	Thr	Asp	Asn 250	Leu	Ile	Pro	Val	Tyr 255	Cys
Ser	Ile	Leu	Ala 260	Ala	Val	Val	Val	Gly 265	Leu	Val	Ala	Tyr	Ile 270	Ala	Phe
Lys	Arg	Trp 275	Asn	Ser	Cys	Lys	Gln 280	Asn	Lys	Gly	Gly	Ala 285	Asn	Ser	Arg
Pro	Val 290	Asn	Gln	Thr	Pro	Pro 295	Pro	Glu	Gly	Glu	Lys 300	Ile	His	Ser	Asp
Ser 305	Gly	Ile	Ser	Val	Asp 310	Ser	Gln	Ser	Leu	His 315	Asp	Gln	Gln	Pro	His 320
Thr	Gln	Thr	Ala	Ser 325	Gly	Gln	Ala	Leu	Lys 330	Gly	Asp	Gly	Gly	Leu 335	Tyr
Ser	Ser	Leu	Pro 340	Pro	Ala	Lys	Arg	Glu 345	Glu	Val	Glu	Lys	Leu 350	Leu	Asn
Gly	Ser	Ala 355	Gly	Asp	Thr	Trp	Arg 360	His	Leu	Ala	Gly	Glu 365	Leu	Gly	Tyr
Gln	Pro 370	Glu	His	Ile	Asp	Ser 375	Phe	Thr	His	Glu	Ala 380	Cys	Pro	Val	Arg
Ala 385	Leu	Leu	Ala	Ser	Trp 390	Ala	Thr	Gln	Asp	Ser 395	Ala	Thr	Leu	Asp	Ala 400

Leu Leu Ala Ala Leu Arg Arg Ile Gln Arg Ala Asp Leu Val Glu Ser  
 405 410 415  
 Leu Cys Ser Glu Ser Thr Ala Thr Ser Pro Val  
 420 425

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Asn Arg Gly Val Pro Phe Arg His Leu Leu Leu Val Leu Gln Leu  
 1 5 10 15  
 Ala Leu Leu Pro Ala Ala Thr Gln Gly Lys Lys Val Val Leu Gly Lys  
 20 25 30  
 Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser  
 35 40 45  
 Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn  
 50 55 60  
 Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala  
 65 70 75 80  
 Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile  
 85 90 95  
 Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu  
 100 105 110  
 Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn  
 115 120 125  
 Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr Ile Thr Leu Glu  
 130 135 140  
 Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly  
 145 150 155 160  
 Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu  
 165 170 175  
 Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys  
 180 185 190  
 Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Phe Gln Lys Ala Ser  
 195 200 205  
 Ser Ile Val Tyr Lys Lys Glu Gly Glu Gln Val Glu Phe Ser Phe Pro  
 210 215 220  
 Leu Ala Phe Thr Val Glu Lys Leu Thr Gly Ser Gly Glu Leu Trp Trp  
 225 230 235 240  
 Gln Ala Glu Arg Ala Ser Ser Ser Lys Ser Trp Ile Thr Phe Asp Leu  
 245 250 255  
 Lys Asn Lys Glu Val Ser Val Lys Arg Val Thr Gln Asp Pro Lys Leu

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met	Asn	Ser	Gly	Val	Ala	Met	Lys	Tyr	Gly	Asn	Asp	Ser	Ser	Ala	Glu
1				5					10					15	
Leu	Ser	Glu	Leu	His	Ser	Ala	Ala	Leu	Ala	Ser	Leu	Lys	Gly	Asp	Ile
			20					25					30		
Val	Glu	Leu	Asn	Lys	Arg	Leu	Gln	Gln	Thr	Glu	Arg	Glu	Asp	Leu	Leu
		35					40					45			
Glu	Lys	Lys	Leu	Ala	Lys	Ala	Gln	Cys	Glu	Gln	Ser	His	Leu	Met	Arg
	50					55					60				
Glu	His	Glu	Asp	Val	Gln	Glu	Arg	Thr	Thr	Leu	Arg	Tyr	Glu	Glu	Arg
65					70					75					80
Ile	Thr	Glu	Leu	His	Ser	Val	Ile	Ala	Glu	Leu	Asn	Lys	Lys	Ile	Asp
				85					90					95	

Arg	Leu	Gln	Gly	Thr	Thr	Ile	Arg	Glu	Glu	Asp	Glu	Tyr	Ser	Glu	Leu	100	105	110
Arg	Ser	Glu	Leu	Ser	Gln	Ser	Gln	His	Glu	Val	Asn	Glu	Asp	Ser	Arg	115	120	125
Ser	Met	Asp	Gln	Asp	Gln	Thr	Ser	Val	Ser	Ile	Pro	Glu	Asn	Gln	Ser	130	135	140
Thr	Met	Val	Thr	Ala	Asp	Met	Asp	Asn	Cys	Ser	Asp	Ile	Asn	Ser	Glu	145	150	155
Leu	Gln	Arg	Val	Leu	Thr	Gly	Leu	Glu	Asn	Val	Val	Cys	Gly	Arg	Lys	165	170	175
Lys	Ser	Ser	Cys	Ser	Leu	Ser	Val	Ala	Glu	Val	Asp	Arg	His	Ile	Glu	180	185	190
Gln	Leu	Thr	Thr	Ala	Ser	Glu	His	Cys	Asp	Leu	Ala	Ile	Lys	Thr	Val	195	200	205
Glu	Glu	Ile	Glu	Gly	Val	Leu	Gly	Arg	Asp	Leu	Tyr	Pro	Asn	Leu	Ala	210	215	220
Glu	Glu	Arg	Ser	Arg	Trp	Glu	Lys	Glu	Leu	Ala	Gly	Leu	Arg	Glu	Glu	225	230	235
Asn	Glu	Ser	Leu	Thr	Ala	Met	Leu	Cys	Ser	Lys	Glu	Glu	Glu	Leu	Asn	245	250	255
Arg	Thr	Lys	Ala	Thr	Met	Asn	Ala	Ile	Arg	Glu	Glu	Arg	Asp	Arg	Leu	260	265	270
Arg	Arg	Arg	Val	Arg	Glu	Leu	Gln	Thr	Arg	Leu	Gln	Ser	Val	Gln	Ala	275	280	285
Thr	Gly	Pro	Ser	Ser	Pro	Gly	Arg	Leu	Thr	Ser	Thr	Asn	Arg	Pro	Ile	290	295	300
Asn	Pro	Ser	Thr	Gly	Glu	Leu	Ser	Thr	Ser	Ser	Ser	Ser	Asn	Asp	Ile	305	310	315
Pro	Ile	Ala	Lys	Ile	Ala	Glu	Arg	Val	Lys	Leu	Ser	Lys	Thr	Arg	Ser	325	330	335
Glu	Ser	Ser	Ser	Ser	Asp	Arg	Pro	Val	Leu	Gly	Ser	Glu	Ile	Ser	Ser	340	345	350
Ile	Gly	Val	Ser	Ser	Ser	Val	Ala	Glu	His	Leu	Ala	His	Ser	Leu	Gln	355	360	365
Asp	Cys	Ser	Asn	Ile	Gln	Glu	Ile	Phe	Gln	Thr	Leu	Tyr	Ser	His	Gly	370	375	380
Ser	Ala	Ile	Ser	Glu	Ser	Lys	Ile	Arg	Glu	Phe	Glu	Val	Glu	Thr	Glu	385	390	395
Arg	Leu	Asn	Ser	Arg	Ile	Glu	His	Leu	Lys	Ser	Gln	Asn	Asp	Leu	Leu	405	410	415
Thr	Ile	Thr	Leu	Glu	Glu	Cys	Lys	Ser	Asn	Ala	Glu	Arg	Met	Ser	Met	420	425	430
Leu	Val	Gly	Lys	Tyr	Glu	Ser	Asn	Ala	Thr	Ala	Leu	Arg	Leu	Ala	Leu	435	440	445
Gln	Tyr	Ser	Glu	Gln	Cys	Ile	Glu	Ala	Tyr	Glu	Leu	Leu	Leu	Ala	Leu	450	455	460

Ala	Glu	Ser	Glu	Gln	Ser	Leu	Ile	Leu	Gly	Gln	Phe	Arg	Ala	Ala	Gly
465					470					475					480
Val	Gly	Ser	Ser	Pro	Gly	Asp	Gln	Ser	Gly	Asp	Glu	Asn	Ile	Thr	Gln
				485					490					495	
Met	Leu	Lys	Arg	Ala	His	Asp	Cys	Arg	Lys	Thr	Ala	Glu	Asn	Ala	Ala
			500					505					510		
Lys	Ala	Leu	Leu	Met	Lys	Leu	Asp	Gly	Ser	Cys	Gly	Gly	Ala	Phe	Ala
		515					520					525			
Val	Ala	Gly	Cys	Ser	Val	Gln	Pro	Trp	Glu	Ser	Leu	Ser	Ser	Asn	Ser
	530					535					540				
His	Thr	Ser	Thr	Thr	Ser	Ser	Thr	Ala	Ser	Ser	Cys	Asp	Thr	Glu	Phe
545					550					555					560
Thr	Lys	Glu	Asp	Glu	Gln	Arg	Leu	Lys	Asp	Tyr	Ile	Gln	Gln	Leu	Lys
				565					570					575	
Asn	Asp	Arg	Ala	Ala	Val	Lys	Leu	Thr	Met	Leu	Glu	Leu	Glu	Ser	Ile
			580					585					590		
His	Ile	Asp	Pro	Leu	Ser	Tyr	Asp	Val	Lys	Pro	Arg	Gly	Asp	Ser	Gln
		595					600					605			
Arg	Leu	Asp	Leu	Glu	Asn	Ala	Val	Leu	Met	Gln	Glu	Leu	Met	Ala	Met
	610					615					620				
Lys	Glu	Glu	Met	Ala	Glu	Leu	Lys	Ala	Gln	Leu	Tyr	Leu	Leu	Glu	Lys
625					630					635					640
Glu	Lys	Lys	Ala	Leu	Glu	Leu	Lys	Leu	Ser	Thr	Arg	Glu	Ala	Gln	Glu
				645					650					655	
Gln	Ala	Tyr	Leu	Val	His	Ile	Glu	His	Leu	Lys	Ser	Glu	Val	Glu	Glu
			660					665					670		
Gln	Lys	Glu	Gln	Arg	Met	Arg	Ser	Leu	Ser	Ser	Thr	Ser	Ser	Gly	Ser
		675					680					685			
Lys	Asp	Lys	Pro	Gly	Lys	Glu	Cys	Ala	Asp	Ala	Ala	Ser	Pro	Ala	Leu
	690					695					700				
Ser	Leu	Ala	Glu	Leu	Arg	Thr	Thr	Cys	Ser	Glu	Asn	Glu	Leu	Ala	Ala
705					710					715					720
Glu	Phe	Thr	Asn	Ala	Ile	Arg	Arg	Glu	Lys	Lys	Leu	Lys	Ala	Arg	Val
			725						730					735	
Gln	Glu	Leu	Val	Ser	Ala	Leu	Glu	Arg	Leu	Thr	Lys	Ser	Ser	Glu	Ile
			740					745					750		
Arg	His	Gln	Gln	Ser	Ala	Glu	Phe	Val	Asn	Asp	Leu	Lys	Arg	Ala	Asn
		755					760					765			
Ser	Asn	Leu	Val	Ala	Ala	Tyr	Glu	Lys	Ala	Lys	Lys	Lys	His	Gln	Asn
	770					775					780				
Lys	Leu	Lys	Lys	Leu	Glu	Ser	Gln	Met	Met	Ala	Met	Val	Glu	Arg	His
785					790					795					800
Glu	Thr	Gln	Val	Arg	Met	Leu	Lys	Gln	Arg	Ile	Ala	Leu	Leu	Glu	Glu
				805					810					815	
Glu	Asn	Ser	Arg	Pro	His	Thr	Asn	Glu	Thr	Ser	Leu				
			820					825							

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 672 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met	Ala	Asp	Val	Phe	Pro	Gly	Asn	Asp	Ser	Thr	Ala	Ser	Gln	Asp	Val	1	5	10	15
Ala	Asn	Arg	Phe	Ala	Arg	Lys	Gly	Ala	Leu	Arg	Gln	Lys	Asn	Val	His	20	25	30	
Glu	Val	Lys	Asp	His	Lys	Phe	Ile	Ala	Arg	Phe	Phe	Lys	Gln	Pro	Thr	35	40	45	
Phe	Cys	Ser	His	Cys	Thr	Asp	Phe	Ile	Trp	Gly	Phe	Gly	Lys	Gly	Gly	50	55	60	
Phe	Gln	Cys	Gln	Val	Cys	Cys	Phe	Val	Val	His	Lys	Arg	Cys	His	Glu	65	70	75	
Phe	Val	Thr	Phe	Ser	Cys	Pro	Gly	Ala	Asp	Lys	Gly	Pro	Asp	Thr	Asp	85	90	95	
Asp	Pro	Arg	Ser	Lys	His	Lys	Phe	Lys	Ile	His	Thr	Tyr	Gly	Ser	Pro	100	105	110	
Thr	Phe	Cys	Asp	His	Cys	Gly	Ser	Leu	Leu	Tyr	Gly	Leu	Ile	His	Gln	115	120	125	
Gly	Met	Lys	Cys	Asp	Thr	Cys	Asp	Met	Asn	Val	His	Lys	Gln	Cys	Val	130	135	140	
Ile	Asn	Val	Pro	Ser	Leu	Cys	Gly	Met	Asp	His	Thr	Glu	Lys	Arg	Gly	145	150	155	
Arg	Ile	Tyr	Leu	Lys	Ala	Glu	Val	Ala	Asp	Glu	Lys	Leu	His	Val	Thr	165	170	175	
Val	Arg	Asp	Ala	Lys	Asn	Leu	Ile	Pro	Met	Asp	Pro	Asn	Gly	Leu	Ser	180	185	190	
Asp	Pro	Tyr	Val	Lys	Leu	Lys	Leu	Ile	Pro	Asp	Pro	Lys	Asn	Glu	Ser	195	200	205	
Lys	Gln	Lys	Thr	Lys	Thr	Ile	Arg	Ser	Thr	Leu	Asn	Pro	Gln	Trp	Asn	210	215	220	
Glu	Ser	Phe	Thr	Phe	Lys	Leu	Lys	Pro	Ser	Asp	Lys	Asp	Arg	Arg	Leu	225	230	235	
Ser	Val	Glu	Ile	Trp	Asp	Trp	Asp	Arg	Thr	Thr	Arg	Asn	Asp	Phe	Met	245	250	255	
Gly	Ser	Leu	Ser	Phe	Gly	Val	Ser	Glu	Leu	Met	Lys	Met	Pro	Ala	Ser	260	265	270	
Gly	Trp	Tyr	Lys	Leu	Leu	Asn	Gln	Glu	Glu	Gly	Glu	Tyr	Tyr	Asn	Val	275	280	285	
Pro	Ile	Pro	Glu	Gly	Asp	Glu	Glu	Gly	Asn	Met	Glu	Leu	Arg	Gln	Lys				

290					295					300					
Phe 305	Glu	Lys	Ala	Lys	Leu 310	Gly	Pro	Ala	Gly	Asn 315	Lys	Val	Ile	Ser	Pro 320
Ser	Glu	Asp	Arg	Lys 325	Gln	Pro	Ser	Asn	Asn 330	Leu	Asp	Arg	Val	Lys 335	Leu
Thr	Asp	Phe	Asn 340	Phe	Leu	Met	Val	Leu 345	Gly	Lys	Gly	Ser	Phe 350	Gly	Lys
Val	Met	Leu 355	Ala	Asp	Arg	Lys	Gly 360	Thr	Glu	Glu	Leu	Tyr 365	Ala	Ile	Lys
Ile	Leu 370	Lys	Lys	Asp	Val	Val 375	Ile	Gln	Asp	Asp 380	Asp	Val	Glu	Cys	Thr
Met 385	Val	Glu	Lys	Arg	Val 390	Leu	Ala	Leu	Leu	Asp 395	Lys	Pro	Pro	Phe	Leu 400
Thr	Gln	Leu	His 405	Ser	Cys	Phe	Gln	Thr	Val 410	Asp	Arg	Leu	Tyr	Phe 415	Val
Met	Glu	Tyr	Val 420	Asn	Gly	Gly	Asp	Leu 425	Met	Tyr	His	Ile	Gln 430	Gln	Val
Gly	Lys	Phe 435	Lys	Glu	Pro	Gln	Ala 440	Val	Phe	Tyr	Ala	Ala 445	Glu	Ile	Ser
Ile	Gly 450	Leu	Phe	Phe	Leu	His 455	Lys	Arg	Gly	Ile	Ile 460	Tyr	Arg	Asp	Leu
Lys 465	Leu	Asp	Asn	Val	Met 470	Leu	Asp	Ser	Glu	Gly 475	His	Ile	Lys	Ile	Ala 480
Asp	Phe	Gly	Met 485	Cys	Lys	Glu	His	Met	Met 490	Asp	Gly	Val	Thr	Thr 495	Arg
Thr	Phe	Cys	Gly 500	Thr	Pro	Asp	Tyr	Ile 505	Ala	Pro	Glu	Ile	Ile 510	Ala	Tyr
Gln	Pro	Tyr 515	Gly	Lys	Ser	Val	Asp 520	Trp	Trp	Ala	Tyr	Gly 525	Val	Leu	Leu
Tyr 530	Glu	Met	Leu	Ala	Gly	Gln 535	Pro	Pro	Phe	Asp	Gly 540	Glu	Asp	Glu	Asp
Glu 545	Leu	Phe	Gln	Ser 550	Ile	Met	Glu	His	Asn 555	Val	Ser	Tyr	Pro	Lys	Ser 560
Leu	Ser	Lys	Glu	Ala 565	Val	Ser	Ile	Cys	Lys 570	Gly	Leu	Met	Thr	Lys 575	His
Pro	Ala	Lys	Arg 580	Leu	Gly	Cys	Gly	Pro 585	Glu	Gly	Glu	Arg	Asp 590	Val	Arg
Glu	His 595	Ala	Phe	Phe	Arg	Arg	Ile 600	Asp	Trp	Glu	Lys	Leu 605	Glu	Asn	Arg
Glu 610	Ile	Gln	Pro	Pro	Phe	Lys 615	Pro	Lys	Val	Cys	Gly 620	Lys	Gly	Ala	Glu
Asn 625	Phe	Asp	Lys	Phe	Phe 630	Thr	Arg	Gly	Gln	Pro 635	Val	Leu	Thr	Pro	Pro 640
Asp	Gln	Leu	Val	Ile 645	Ala	Asn	Ile	Asp	Gln 650	Ser	Asp	Phe	Glu	Gly 655	Phe

Ser Tyr Val Asn Pro Gln Phe Val His Pro Ile Leu Gln Ser Ala Val  
660 665 670

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 471 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met	Asp	Ile	Leu	Cys	Glu	Glu	Asn	Thr	Ser	Leu	Ser	Ser	Thr	Thr	Asn	1	5	10	15
Ser	Leu	Met	Gln	Leu	Asn	Asp	Asp	Thr	Arg	Leu	Tyr	Ser	Asn	Asp	Phe	20	25	30	
Asn	Ser	Gly	Glu	Ala	Asn	Thr	Ser	Asp	Ala	Phe	Asn	Trp	Thr	Val	Asp	35	40	45	
Ser	Glu	Asn	Arg	Thr	Asn	Leu	Ser	Cys	Glu	Gly	Cys	Leu	Ser	Pro	Ser	50	55	60	
Cys	Leu	Ser	Leu	Leu	His	Leu	Gln	Glu	Lys	Asn	Trp	Ser	Ala	Leu	Leu	65	70	75	80
Thr	Ala	Val	Val	Ile	Ile	Leu	Thr	Ile	Ala	Gly	Asn	Ile	Leu	Val	Ile	85	90	95	
Met	Ala	Val	Ser	Leu	Glu	Lys	Lys	Leu	Gln	Asn	Ala	Thr	Asn	Tyr	Phe	100	105	110	
Leu	Met	Ser	Leu	Ala	Ile	Ala	Asp	Met	Leu	Leu	Gly	Phe	Leu	Val	Met	115	120	125	
Pro	Val	Ser	Met	Leu	Thr	Ile	Leu	Tyr	Gly	Tyr	Arg	Trp	Pro	Leu	Pro	130	135	140	
Ser	Lys	Leu	Cys	Ala	Val	Trp	Ile	Tyr	Leu	Asp	Val	Leu	Phe	Ser	Thr	145	150	155	160
Ala	Ser	Ile	Met	His	Leu	Cys	Ala	Ile	Ser	Leu	Asp	Arg	Tyr	Val	Ala	165	170	175	
Ile	Gln	Asn	Pro	Ile	His	His	Ser	Arg	Phe	Asn	Ser	Arg	Thr	Lys	Ala	180	185	190	
Phe	Leu	Lys	Ile	Ile	Ala	Val	Trp	Thr	Ile	Ser	Val	Gly	Ile	Ser	Met	195	200	205	
Pro	Ile	Pro	Val	Phe	Gly	Leu	Gln	Asp	Asp	Ser	Lys	Val	Phe	Lys	Glu	210	215	220	
Gly	Ser	Cys	Leu	Leu	Ala	Asp	Asp	Asn	Phe	Val	Leu	Ile	Gly	Ser	Phe	225	230	235	240
Val	Ser	Phe	Phe	Ile	Pro	Leu	Thr	Ile	Met	Val	Ile	Thr	Tyr	Phe	Leu	245	250	255	
Thr	Ile	Lys	Ser	Leu	Gln	Lys	Glu	Ala	Thr	Leu	Cys	Val	Ser	Asp	Leu	260	265	270	

Gly Thr Arg Ala Lys Leu Ala Ser Phe Ser Phe Leu Pro Gln Ser Ser  
275 280 285  
Leu Ser Ser Glu Lys Leu Phe Gln Arg Ser Ile His Arg Glu Pro Gly  
290 295 300  
Ser Tyr Thr Gly Arg Arg Thr Met Gln Ser Ile Ser Asn Glu Gln Lys  
305 310 315 320  
Ala Cys Lys Val Leu Gly Ile Val Phe Phe Leu Phe Val Val Met Trp  
325 330 335  
Cys Pro Phe Phe Ile Thr Asn Ile Met Ala Val Ile Cys Lys Glu Ser  
340 345 350  
Cys Asn Glu Asp Val Ile Gly Ala Leu Leu Asn Val Phe Val Trp Ile  
355 360 365  
Gly Tyr Leu Ser Ser Ala Val Asn Pro Leu Val Tyr Thr Leu Phe Asn  
370 375 380  
Lys Thr Tyr Arg Ser Ala Phe Ser Arg Tyr Ile Gln Cys Gln Tyr Lys  
385 390 395 400  
Glu Asn Lys Lys Pro Leu Gln Leu Ile Leu Val Asn Thr Ile Pro Ala  
405 410 415  
Leu Ala Tyr Lys Ser Ser Gln Leu Gln Met Gly Gln Lys Lys Asn Ser  
420 425 430  
Lys Gln Asp Ala Lys Thr Thr Asp Asn Asp Cys Ser Met Val Ala Leu  
435 440 445  
Gly Lys Gln His Ser Glu Glu Ala Ser Lys Asp Asn Ser Asp Gly Val  
450 455 460  
Asn Glu Lys Val Ser Cys Val  
465 470

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Ala Leu Ser Tyr Arg Val Ser Glu Leu Gln Ser Thr Ile Pro Glu  
1 5 10 15  
His Ile Leu Gln Ser Thr Phe Val His Val Ile Ser Ser Asn Trp Ser  
20 25 30  
Gly Leu Gln Thr Glu Ser Ile Pro Glu Glu Met Lys Gln Ile Val Glu  
35 40 45  
Glu Gln Gly Asn Lys Leu His Trp Ala Ala Leu Leu Ile Leu Met Val  
50 55 60  
Ile Ile Pro Thr Ile Gly Gly Asn Thr Leu Val Ile Leu Ala Val Ser  
65 70 75 80  
Leu Glu Lys Lys Leu Gln Tyr Ala Thr Asn Tyr Phe Leu Met Ser Leu

				85				90				95			
Ala	Val	Ala	Asp 100	Leu	Leu	Val	Gly	Leu 105	Phe	Val	Met	Pro	Ile 110	Ala	Leu
Leu	Thr	Ile 115	Met	Phe	Glu	Ala	Met 120	Trp	Pro	Leu	Pro	Leu 125	Val	Leu	Cys
Pro	Ala 130	Trp	Leu	Phe	Leu	Asp 135	Val	Leu	Phe	Ser	Thr 140	Ala	Ser	Ile	Met
His 145	Leu	Cys	Ala	Ile	Ser 150	Val	Asp	Arg	Tyr	Ile 155	Ala	Ile	Lys	Lys	Pro 160
Ile	Gln	Ala	Asn	Gln 165	Tyr	Asn	Ser	Arg	Ala 170	Thr	Ala	Phe	Ile	Lys 175	Ile
Thr	Val	Val	Trp 180	Leu	Ile	Ser	Ile	Gly 185	Ile	Ala	Ile	Pro	Val 190	Pro	Ile
Lys	Gly	Ile 195	Glu	Thr	Asp	Val	Asp 200	Asn	Pro	Asn	Asn	Ile 205	Thr	Cys	Val
Leu	Thr 210	Lys	Glu	Arg	Phe	Gly 215	Asp	Phe	Met	Leu	Phe 220	Gly	Ser	Leu	Ala
Ala 225	Phe	Phe	Thr	Pro	Leu 230	Ala	Ile	Met	Ile	Val 235	Thr	Tyr	Phe	Leu	Thr 240
Ile	His	Ala	Leu	Gln 245	Lys	Lys	Ala	Tyr	Leu 250	Val	Lys	Asn	Lys	Pro 255	Pro
Gln	Arg	Leu	Thr 260	Trp	Leu	Thr	Val	Ser 265	Thr	Val	Phe	Gln	Arg 270	Asp	Glu
Thr	Pro	Cys 275	Ser	Ser	Pro	Glu	Lys 280	Val	Ala	Met	Leu	Asp 285	Gly	Ser	Arg
Lys	Asp 290	Lys	Ala	Leu	Pro	Asn 295	Ser	Gly	Asp	Glu	Thr 300	Leu	Met	Arg	Arg
Thr 305	Ser	Thr	Ile	Gly	Lys 310	Lys	Ser	Val	Gln	Thr 315	Ile	Ser	Asn	Glu	Gln 320
Arg	Ala	Ser	Lys	Val 325	Leu	Gly	Ile	Val	Phe 330	Phe	Leu	Phe	Leu	Leu 335	Met
Trp	Cys	Pro	Phe 340	Phe	Ile	Thr	Asn 345	Ile	Thr	Leu	Val	Leu	Cys 350	Asp	Ser
Cys	Asn	Gln 355	Thr	Thr	Leu	Gln	Met 360	Leu	Leu	Glu	Ile	Phe 365	Val	Trp	Ile
Gly	Tyr 370	Val	Ser	Ser	Gly	Val 375	Asn	Pro	Leu	Val	Tyr 380	Thr	Leu	Phe	Asn
Lys 385	Thr	Phe	Arg	Asp	Ala 390	Phe	Gly	Arg	Tyr	Ile 395	Thr	Cys	Asn	Tyr	Arg 400
Ala	Thr	Lys	Ser	Val 405	Lys	Thr	Leu	Arg	Lys 410	Arg	Ser	Ser	Lys	Ile 415	Tyr
Phe	Arg	Asn	Pro 420	Met	Ala	Glu	Asn 425	Ser	Lys	Phe	Phe	Lys	Lys 430	His	Gly
Ile	Arg	Asn 435	Gly	Ile	Asn	Pro	Ala 440	Met	Tyr	Gln	Ser	Pro 445	Met	Arg	Leu

Arg Ser Ser Thr Ile Gln Ser Ser Ser Ile Ile Leu Leu Asp Thr Leu  
 450 455 460  
 Leu Leu Thr Glu Asn Glu Gly Asp Lys Thr Glu Glu Gln Val Ser Val  
 465 470 475 480  
 Val

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2843 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Ala Ala Ala Ser Tyr Asp Gln Leu Leu Lys Gln Val Glu Ala Leu  
 1 5 10 15  
 Lys Met Glu Asn Ser Asn Leu Arg Gln Glu Leu Glu Asp Asn Ser Asn  
 20 25 30  
 His Leu Thr Lys Leu Glu Thr Glu Ala Ser Asn Met Lys Glu Val Leu  
 35 40 45  
 Lys Gln Leu Gln Gly Ser Ile Glu Asp Glu Ala Met Ala Ser Ser Gly  
 50 55 60  
 Gln Ile Asp Leu Leu Glu Arg Leu Lys Glu Leu Asn Leu Asp Ser Ser  
 65 70 75 80  
 Asn Phe Pro Gly Val Lys Leu Arg Ser Lys Met Ser Leu Arg Ser Tyr  
 85 90 95  
 Gly Ser Arg Glu Gly Ser Val Ser Ser Arg Ser Gly Glu Cys Ser Pro  
 100 105 110  
 Val Pro Met Gly Ser Phe Pro Arg Arg Gly Phe Val Asn Gly Ser Arg  
 115 120 125  
 Glu Ser Thr Gly Tyr Leu Glu Glu Leu Glu Lys Glu Arg Ser Leu Leu  
 130 135 140  
 Leu Ala Asp Leu Asp Lys Glu Glu Lys Glu Lys Asp Trp Tyr Tyr Ala  
 145 150 155 160  
 Gln Leu Gln Asn Leu Thr Lys Arg Ile Asp Ser Leu Pro Leu Thr Glu  
 165 170 175  
 Asn Phe Ser Leu Gln Thr Asp Met Thr Arg Arg Gln Leu Glu Tyr Glu  
 180 185 190  
 Ala Arg Gln Ile Arg Val Ala Met Glu Glu Gln Leu Gly Thr Cys Gln  
 195 200 205  
 Asp Met Glu Lys Arg Ala Gln Arg Arg Ile Ala Arg Ile Gln Gln Ile  
 210 215 220  
 Glu Lys Asp Ile Leu Arg Ile Arg Gln Leu Leu Gln Ser Gln Ala Thr  
 225 230 235 240  
 Glu Ala Glu Arg Ser Ser Gln Asn Lys His Glu Thr Gly Ser His Asp  
 245 250 255

Ala	Glu	Arg	Gln	Asn	Glu	Gly	Gln	Gly	Val	Gly	Glu	Ile	Asn	Met	Ala	
			260					265					270			
Thr	Ser	Gly	Asn	Gly	Gln	Gly	Ser	Thr	Thr	Arg	Met	Asp	His	Glu	Thr	
		275					280					285				
Ala	Ser	Val	Leu	Ser	Ser	Ser	Ser	Thr	His	Ser	Ala	Pro	Arg	Arg	Leu	
	290					295					300					
Thr	Ser	His	Leu	Gly	Thr	Lys	Val	Glu	Met	Val	Tyr	Ser	Leu	Leu	Ser	
305					310					315					320	
Met	Leu	Gly	Thr	His	Asp	Lys	Asp	Asp	Met	Ser	Arg	Thr	Leu	Leu	Ala	
				325					330						335	
Met	Ser	Ser	Ser	Gln	Asp	Ser	Cys	Ile	Ser	Met	Arg	Gln	Ser	Gly	Cys	
			340					345					350			
Leu	Pro	Leu	Leu	Ile	Gln	Leu	Leu	His	Gly	Asn	Asp	Lys	Asp	Ser	Val	
		355					360					365				
Leu	Leu	Gly	Asn	Ser	Arg	Gly	Ser	Lys	Glu	Ala	Arg	Ala	Arg	Ala	Ser	
	370					375					380					
Ala	Ala	Leu	His	Asn	Ile	Ile	His	Ser	Gln	Pro	Asp	Asp	Lys	Arg	Gly	
385					390					395					400	
Arg	Arg	Glu	Ile	Arg	Val	Leu	His	Leu	Leu	Glu	Gln	Ile	Arg	Ala	Tyr	
				405					410					415		
Cys	Ser	Thr	Cys	Trp	Glu	Trp	Gln	Glu	Ala	His	Glu	Pro	Gly	Met	Asp	
			420					425					430			
Gln	Asp	Lys	Asn	Pro	Met	Pro	Ala	Pro	Val	Glu	His	Gln	Ile	Cys	Pro	
	435						440					445				
Ala	Val	Cys	Val	Leu	Met	Lys	Leu	Ser	Phe	Asp	Glu	Glu	His	Arg	His	
	450					455					460					
Ala	Met	Asn	Glu	Leu	Gly	Gly	Leu	Gln	Ala	Ile	Ala	Glu	Leu	Leu	Gln	
465					470					475					480	
Val	Asp	Cys	Glu	Met	Tyr	Gly	Leu	Thr	Asn	Asp	His	Tyr	Ser	Ile	Thr	
				485					490					495		
Leu	Arg	Arg	Tyr	Ala	Gly	Met	Ala	Leu	Thr	Asn	Leu	Thr	Phe	Gly	Asp	
			500				505						510			
Val	Ala	Asn	Lys	Ala	Thr	Leu	Cys	Ser	Met	Lys	Gly	Cys	Met	Arg	Ala	
		515					520					525				
Leu	Val	Ala	Gln	Leu	Lys	Ser	Glu	Ser	Glu	Asp	Leu	Gln	Gln	Val	Ile	
	530					535					540					
Ala	Ser	Val	Leu	Arg	Asn	Leu	Ser	Trp	Arg	Ala	Asp	Val	Asn	Ser	Lys	
545					550					555					560	
Lys	Thr	Leu	Arg	Glu	Val	Gly	Ser	Val	Lys	Ala	Leu	Met	Glu	Cys	Ala	
				565					570					575		
Leu	Glu	Val	Lys	Lys	Glu	Ser	Thr	Leu	Lys	Ser	Val	Leu	Ser	Ala	Leu	
			580				585					590				
Trp	Asn	Leu	Ser	Ala	His	Cys	Thr	Glu	Asn	Lys	Ala	Asp	Ile	Cys	Ala	
		595					600					605				
Val	Asp	Gly	Ala	Leu	Ala	Phe	Leu	Val	Gly	Thr	Leu	Thr	Tyr	Arg	Ser	
	610					615					620					

Gln	Thr	Asn	Thr	Leu	Ala	Ile	Ile	Glu	Ser	Gly	Gly	Gly	Ile	Leu	Arg	625	630	635	640
Asn	Val	Ser	Ser	Leu	Ile	Ala	Thr	Asn	Glu	Asp	His	Arg	Gln	Ile	Leu	645	650	655	
Arg	Glu	Asn	Asn	Cys	Leu	Gln	Thr	Leu	Leu	Gln	His	Leu	Lys	Ser	His	660	665	670	
Ser	Leu	Thr	Ile	Val	Ser	Asn	Ala	Cys	Gly	Thr	Leu	Trp	Asn	Leu	Ser	675	680	685	
Ala	Arg	Asn	Pro	Lys	Asp	Gln	Glu	Ala	Leu	Trp	Asp	Met	Gly	Ala	Val	690	695	700	
Ser	Met	Leu	Lys	Asn	Leu	Ile	His	Ser	Lys	His	Lys	Met	Ile	Ala	Met	705	710	715	720
Gly	Ser	Ala	Ala	Ala	Leu	Arg	Asn	Leu	Met	Ala	Asn	Arg	Pro	Ala	Lys	725	730	735	
Tyr	Lys	Asp	Ala	Asn	Ile	Met	Ser	Pro	Gly	Ser	Ser	Leu	Pro	Ser	Leu	740	745	750	
His	Val	Arg	Lys	Gln	Lys	Ala	Leu	Glu	Ala	Glu	Leu	Asp	Ala	Gln	His	755	760	765	
Leu	Ser	Glu	Thr	Phe	Asp	Asn	Ile	Asp	Asn	Ile	Ser	Pro	Lys	Ala	Ser	770	775	780	
His	Arg	Ser	Lys	Gln	Arg	His	Lys	Gln	Ser	Leu	Tyr	Gly	Asp	Tyr	Val	785	790	795	800
Phe	Asp	Thr	Asn	Arg	His	Asp	Asp	Asn	Arg	Ser	Asp	Asn	Phe	Asn	Thr	805	810	815	
Gly	Asn	Met	Thr	Val	Leu	Ser	Pro	Tyr	Leu	Asn	Thr	Thr	Val	Leu	Pro	820	825	830	
Ser	Ser	Ser	Ser	Ser	Arg	Gly	Ser	Leu	Asp	Ser	Ser	Arg	Ser	Glu	Lys	835	840	845	
Asp	Arg	Ser	Leu	Glu	Arg	Glu	Arg	Gly	Ile	Gly	Leu	Gly	Asn	Tyr	His	850	855	860	
Pro	Ala	Thr	Glu	Asn	Pro	Gly	Thr	Ser	Ser	Lys	Arg	Gly	Leu	Gln	Ile	865	870	875	880
Ser	Thr	Thr	Ala	Ala	Gln	Ile	Ala	Lys	Val	Met	Glu	Glu	Val	Ser	Ala	885	890	895	
Ile	His	Thr	Ser	Gln	Glu	Asp	Arg	Ser	Ser	Gly	Ser	Thr	Thr	Glu	Leu	900	905	910	
His	Cys	Val	Thr	Asp	Glu	Arg	Asn	Ala	Leu	Arg	Arg	Ser	Ser	Ala	Ala	915	920	925	
His	Thr	His	Ser	Asn	Thr	Tyr	Asn	Phe	Thr	Lys	Ser	Glu	Asn	Ser	Asn	930	935	940	
Arg	Thr	Cys	Ser	Met	Pro	Tyr	Ala	Lys	Leu	Glu	Tyr	Lys	Arg	Ser	Ser	945	950	955	960
Asn	Asp	Ser	Leu	Asn	Ser	Val	Ser	Ser	Ser	Asp	Gly	Tyr	Gly	Lys	Arg	965	970	975	
Gly	Gln	Met	Lys	Pro	Ser	Ile	Glu	Ser	Tyr	Ser	Glu	Asp	Asp	Glu	Ser	980	985	990	

Lys Phe Cys Ser Tyr Gly Gln Tyr Pro Ala Asp Leu Ala His Lys Ile  
 995 1000 1005  
 His Ser Ala Asn His Met Asp Asp Asn Asp Gly Glu Leu Asp Thr Pro  
 1010 1015 1020  
 Ile Asn Tyr Ser Leu Lys Tyr Ser Asp Glu Gln Leu Asn Ser Gly Arg  
 1025 1030 1035 1040  
 Gln Ser Pro Ser Gln Asn Glu Arg Trp Ala Arg Pro Lys His Ile Ile  
 1045 1050 1055  
 Glu Asp Glu Ile Lys Gln Ser Glu Gln Arg Gln Ser Arg Asn Gln Ser  
 1060 1065 1070  
 Thr Thr Tyr Pro Val Tyr Thr Glu Ser Thr Asp Asp Lys His Leu Lys  
 1075 1080 1085  
 Phe Gln Pro His Phe Gly Gln Gln Glu Cys Val Ser Pro Tyr Arg Ser  
 1090 1095 1100  
 Arg Gly Ala Asn Gly Ser Glu Thr Asn Arg Val Gly Ser Asn His Gly  
 1105 1110 1115 1120  
 Ile Asn Gln Asn Val Ser Gln Ser Leu Cys Gln Glu Asp Asp Tyr Glu  
 1125 1130 1135  
 Asp Asp Lys Pro Thr Asn Tyr Ser Glu Arg Tyr Ser Glu Glu Glu Gln  
 1140 1145 1150  
 His Glu Glu Glu Glu Arg Pro Thr Asn Tyr Ser Ile Lys Tyr Asn Glu  
 1155 1160 1165  
 Glu Lys Arg His Val Asp Gln Pro Ile Asp Tyr Ser Ile Leu Lys Ala  
 1170 1175 1180  
 Thr Asp Ile Pro Ser Ser Gln Lys Gln Ser Phe Ser Phe Ser Lys Ser  
 1185 1190 1195 1200  
 Ser Ser Gly Gln Ser Ser Lys Thr Glu His Met Ser Ser Ser Ser Glu  
 1205 1210 1215  
 Asn Thr Ser Thr Pro Ser Ser Asn Ala Lys Arg Gln Asn Gln Leu His  
 1220 1225 1230  
 Pro Ser Ser Ala Gln Ser Arg Ser Gly Gln Pro Gln Lys Ala Ala Thr  
 1235 1240 1245  
 Cys Lys Val Ser Ser Ile Asn Gln Glu Thr Ile Gln Thr Tyr Cys Val  
 1250 1255 1260  
 Glu Asp Thr Pro Ile Cys Phe Ser Arg Cys Ser Ser Leu Ser Ser Leu  
 1265 1270 1275 1280  
 Ser Ser Ala Glu Asp Glu Ile Gly Cys Asn Gln Thr Thr Gln Glu Ala  
 1285 1290 1295  
 Asp Ser Ala Asn Thr Leu Gln Ile Ala Glu Ile Lys Glu Lys Ile Gly  
 1300 1305 1310  
 Thr Arg Ser Ala Glu Asp Pro Val Ser Glu Val Pro Ala Val Ser Gln  
 1315 1320 1325  
 His Pro Arg Thr Lys Ser Ser Arg Leu Gln Gly Ser Ser Leu Ser Ser  
 1330 1335 1340  
 Glu Ser Ala Arg His Lys Ala Val Glu Phe Ser Ser Gly Ala Lys Ser  
 1345 1350 1355 1360

Pro Ser Lys Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr  
1365 1370 1375

Val Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val Ser Ser  
1380 1385 1390

Leu Asp Ser Phe Glu Ser Arg Ser Ile Ala Ser Ser Val Gln Ser Glu  
1395 1400 1405

Pro Cys Ser Gly Met Val Ser Gly Ile Ile Ser Pro Ser Asp Leu Pro  
1410 1415 1420

Asp Ser Pro Gly Gln Thr Met Pro Pro Ser Arg Ser Lys Thr Pro Pro  
1425 1430 1435 1440

Pro Pro Pro Gln Thr Ala Gln Thr Lys Arg Glu Val Pro Lys Asn Lys  
1445 1450 1455

Ala Pro Thr Ala Glu Lys Arg Glu Ser Gly Pro Lys Gln Ala Ala Val  
1460 1465 1470

Asn Ala Ala Val Gln Arg Val Gln Val Leu Pro Asp Ala Asp Thr Leu  
1475 1480 1485

Leu His Phe Ala Thr Glu Ser Thr Pro Asp Gly Phe Ser Cys Ser Ser  
1490 1495 1500

Ser Leu Ser Ala Leu Ser Leu Asp Glu Pro Phe Ile Gln Lys Asp Val  
1505 1510 1515 1520

Glu Leu Arg Ile Met Pro Pro Val Gln Glu Asn Asp Asn Gly Asn Glu  
1525 1530 1535

Thr Glu Ser Glu Gln Pro Lys Glu Ser Asn Glu Asn Gln Glu Lys Glu  
1540 1545 1550

Ala Glu Lys Thr Ile Asp Ser Glu Lys Asp Leu Leu Asp Asp Ser Asp  
1555 1560 1565

Asp Asp Asp Ile Glu Ile Leu Glu Glu Cys Ile Ile Ser Ala Met Pro  
1570 1575 1580

Thr Lys Ser Ser Arg Lys Ala Lys Lys Pro Ala Gln Thr Ala Ser Lys  
1585 1590 1595 1600

Leu Pro Pro Pro Val Ala Arg Lys Pro Ser Gln Leu Pro Val Tyr Lys  
1605 1610 1615

Leu Leu Pro Ser Gln Asn Arg Leu Gln Pro Gln Lys His Val Ser Phe  
1620 1625 1630

Thr Pro Gly Asp Asp Met Pro Arg Val Tyr Cys Val Glu Gly Thr Pro  
1635 1640 1645

Ile Asn Phe Ser Thr Ala Thr Ser Leu Ser Asp Leu Thr Ile Glu Ser  
1650 1655 1660

Pro Pro Asn Glu Leu Ala Ala Gly Glu Gly Val Arg Gly Gly Ala Gln  
1665 1670 1675 1680

Ser Gly Glu Phe Glu Lys Arg Asp Thr Ile Pro Thr Glu Gly Arg Ser  
1685 1690 1695

Thr Asp Glu Ala Gln Gly Gly Lys Thr Ser Ser Val Thr Ile Pro Glu  
1700 1705 1710

Leu Asp Asp Asn Lys Ala Glu Glu Gly Asp Ile Leu Ala Glu Cys Ile  
1715 1720 1725

Asn 1730	Ser	Ala	Met	Pro	Lys	Gly	Lys	Ser	His	Lys	Pro	Phe	Arg	Val	Lys	
						1735					1740					
Lys 1745	Ile	Met	Asp	Gln	Val	Gln	Gln	Ala	Ser	Ala	Ser	Ser	Ser	Ala	Pro	
					1750					1755					1760	
Asn 1765	Lys	Asn	Gln	Leu	Asp	Gly	Lys	Lys	Lys	Lys	Pro	Thr	Ser	Pro	Val	
				1765					1770					1775		
Lys 1780	Pro	Ile	Pro	Gln	Asn	Thr	Glu	Tyr	Arg	Thr	Arg	Val	Arg	Lys	Asn	
			1780				1785						1790			
Ala 1795	Asp	Ser	Lys	Asn	Asn	Leu	Asn	Ala	Glu	Arg	Val	Phe	Ser	Asp	Asn	
			1795				1800					1805				
Lys 1810	Asp	Ser	Lys	Lys	Gln	Asn	Leu	Lys	Asn	Asn	Ser	Lys	Asp	Phe	Asn	
					1815					1820						
Asp 1825	Lys	Leu	Pro	Asn	Asn	Glu	Asp	Arg	Val	Arg	Gly	Ser	Phe	Ala	Phe	
					1830					1835					1840	
Asp 1845	Ser	Pro	His	His	Tyr	Thr	Pro	Ile	Glu	Gly	Thr	Pro	Tyr	Cys	Phe	
				1845					1850					1855		
Ser 1860	Arg	Asn	Asp	Ser	Leu	Ser	Ser	Leu	Asp	Phe	Asp	Asp	Asp	Asp	Val	
			1860					1865					1870			
Asp 1875	Leu	Ser	Arg	Glu	Lys	Ala	Glu	Leu	Arg	Lys	Ala	Lys	Glu	Asn	Lys	
						1880						1885				
Glu 1890	Ser	Glu	Ala	Lys	Val	Thr	Ser	His	Thr	Glu	Leu	Thr	Ser	Asn	Gln	
						1895					1900					
Gln 1905	Ser	Ala	Asn	Lys	Thr	Gln	Ala	Ile	Ala	Lys	Gln	Pro	Ile	Asn	Arg	
					1910					1915					1920	
Gly 1925	Gln	Pro	Lys	Pro	Ile	Leu	Gln	Lys	Gln	Ser	Thr	Phe	Pro	Gln	Ser	
				1925					1930					1935		
Ser 1940	Lys	Asp	Ile	Pro	Asp	Arg	Gly	Ala	Ala	Thr	Asp	Glu	Lys	Leu	Gln	
			1940					1945					1950			
Asn 1955	Phe	Ala	Ile	Glu	Asn	Thr	Pro	Val	Cys	Phe	Ser	His	Asn	Ser	Ser	
			1955				1960					1965				
Leu 1970	Ser	Ser	Leu	Ser	Asp	Ile	Asp	Gln	Glu	Asn	Asn	Asn	Lys	Glu	Asn	
					1975					1980						
Glu 1985	Pro	Ile	Lys	Glu	Thr	Glu	Pro	Pro	Asp	Ser	Gln	Gly	Glu	Pro	Ser	
					1990				1995					2000		
Lys 2005	Pro	Gln	Ala	Ser	Gly	Tyr	Ala	Pro	Lys	Ser	Phe	His	Val	Glu	Asp	
				2005				2010						2015		
Thr 2020	Pro	Val	Cys	Phe	Ser	Arg	Asn	Ser	Ser	Leu	Ser	Ser	Leu	Ser	Ile	
			2020				2025						2030			
Asp 2035	Ser	Glu	Asp	Asp	Leu	Leu	Gln	Glu	Cys	Ile	Ser	Ser	Ala	Met	Pro	
						2040					2045					
Lys 2050	Lys	Lys	Lys	Pro	Ser	Arg	Leu	Lys	Gly	Asp	Asn	Glu	Lys	His	Ser	
						2055				2060						
Pro 2065	Arg	Asn	Met	Gly	Gly	Ile	Leu	Gly	Glu	Asp	Leu	Thr	Leu	Asp	Leu	
					2070				2075						2080	
Lys 2085	Asp	Ile	Gln	Arg	Pro	Asp	Ser	Glu	His	Gly	Leu	Ser	Pro	Asp	Ser	
				2085				2090						2095		

Glu	Asn	Phe	Asp	Trp	Lys	Ala	Ile	Gln	Glu	Gly	Ala	Asn	Ser	Ile	Val	2100	2105	2110
Ser	Ser	Leu	His	Gln	Ala	Ala	Ala	Ala	Ala	Cys	Leu	Ser	Arg	Gln	Ala	2115	2120	2125
Ser	Ser	Asp	Ser	Asp	Ser	Ile	Leu	Ser	Leu	Lys	Ser	Gly	Ile	Ser	Leu	2130	2135	2140
Gly	Ser	Pro	Phe	His	Leu	Thr	Pro	Asp	Gln	Glu	Glu	Lys	Pro	Phe	Thr	2145	2150	2155
Ser	Asn	Lys	Gly	Pro	Arg	Ile	Leu	Lys	Pro	Gly	Glu	Lys	Ser	Thr	Leu	2165	2170	2175
Glu	Thr	Lys	Lys	Ile	Glu	Ser	Glu	Ser	Lys	Gly	Ile	Lys	Gly	Gly	Lys	2180	2185	2190
Lys	Val	Tyr	Lys	Ser	Leu	Ile	Thr	Gly	Lys	Val	Arg	Ser	Asn	Ser	Glu	2195	2200	2205
Ile	Ser	Gly	Gln	Met	Lys	Gln	Pro	Leu	Gln	Ala	Asn	Met	Pro	Ser	Ile	2210	2215	2220
Ser	Arg	Gly	Arg	Thr	Met	Ile	His	Ile	Pro	Gly	Val	Arg	Asn	Ser	Ser	2225	2230	2235
Ser	Ser	Thr	Ser	Pro	Val	Ser	Lys	Lys	Gly	Pro	Pro	Leu	Lys	Thr	Pro	2245	2250	2255
Ala	Ser	Lys	Ser	Pro	Ser	Glu	Gly	Gln	Thr	Ala	Thr	Thr	Ser	Pro	Arg	2260	2265	2270
Gly	Ala	Lys	Pro	Ser	Val	Lys	Ser	Glu	Leu	Ser	Pro	Val	Ala	Arg	Gln	2275	2280	2285
Thr	Ser	Gln	Ile	Gly	Gly	Ser	Ser	Lys	Ala	Pro	Ser	Arg	Ser	Gly	Ser	2290	2295	2300
Arg	Asp	Ser	Thr	Pro	Ser	Arg	Pro	Ala	Gln	Gln	Pro	Leu	Ser	Arg	Pro	2305	2310	2315
Ile	Gln	Ser	Pro	Gly	Arg	Asn	Ser	Ile	Ser	Pro	Gly	Arg	Asn	Gly	Ile	2325	2330	2335
Ser	Pro	Pro	Asn	Lys	Ile	Ser	Gln	Leu	Pro	Arg	Thr	Ser	Ser	Pro	Ser	2340	2345	2350
Thr	Ala	Ser	Thr	Lys	Ser	Ser	Gly	Ser	Gly	Lys	Met	Ser	Tyr	Thr	Ser	2355	2360	2365
Pro	Gly	Arg	Gln	Met	Ser	Gln	Gln	Asn	Leu	Thr	Lys	Gln	Thr	Gly	Leu	2370	2375	2380
Ser	Lys	Asn	Ala	Ser	Ser	Ile	Pro	Arg	Ser	Glu	Ser	Ala	Ser	Lys	Gly	2385	2390	2395
Leu	Asn	Gln	Met	Asn	Asn	Gly	Asn	Gly	Ala	Asn	Lys	Lys	Val	Glu	Leu	2405	2410	2415
Ser	Arg	Met	Ser	Ser	Thr	Lys	Ser	Ser	Gly	Ser	Glu	Ser	Asp	Arg	Ser	2420	2425	2430
Glu	Arg	Pro	Val	Leu	Val	Arg	Gln	Ser	Thr	Phe	Ile	Lys	Glu	Ala	Pro	2435	2440	2445
Ser	Pro	Thr	Leu	Arg	Arg	Lys	Leu	Glu	Glu	Ser	Ala	Ser	Phe	Glu	Ser	2450	2455	2460

Leu	Ser	Pro	Ser	Ser	Arg	Pro	Ala	Ser	Pro	Thr	Arg	Ser	Gln	Ala	Gln	2465	2470	2475	2480
Thr	Pro	Val	Leu	Ser	Pro	Ser	Leu	Pro	Asp	Met	Ser	Leu	Ser	Thr	His	2485	2490	2495	
Ser	Ser	Val	Gln	Ala	Gly	Gly	Trp	Arg	Lys	Leu	Pro	Pro	Asn	Leu	Ser	2500	2505	2510	
Pro	Thr	Ile	Glu	Tyr	Asn	Asp	Gly	Arg	Pro	Ala	Lys	Arg	His	Asp	Ile	2515	2520	2525	
Ala	Arg	Ser	His	Ser	Glu	Ser	Pro	Ser	Arg	Leu	Pro	Ile	Asn	Arg	Ser	2530	2535	2540	
Gly	Thr	Trp	Lys	Arg	Glu	His	Ser	Lys	His	Ser	Ser	Ser	Leu	Pro	Arg	2545	2550	2555	2560
Val	Ser	Thr	Trp	Arg	Arg	Thr	Gly	Ser	Ser	Ser	Ser	Ile	Leu	Ser	Ala	2565	2570	2575	
Ser	Ser	Glu	Ser	Ser	Glu	Lys	Ala	Lys	Ser	Glu	Asp	Glu	Lys	His	Val	2580	2585	2590	
Asn	Ser	Ile	Ser	Gly	Thr	Lys	Gln	Ser	Lys	Glu	Asn	Gln	Val	Ser	Ala	2595	2600	2605	
Lys	Gly	Thr	Trp	Arg	Lys	Ile	Lys	Glu	Asn	Glu	Phe	Ser	Pro	Thr	Asn	2610	2615	2620	
Ser	Thr	Ser	Gln	Thr	Val	Ser	Ser	Gly	Ala	Thr	Asn	Gly	Ala	Glu	Ser	2625	2630	2635	2640
Lys	Thr	Leu	Ile	Tyr	Gln	Met	Ala	Pro	Ala	Val	Ser	Lys	Thr	Glu	Asp	2645	2650	2655	
Val	Trp	Val	Arg	Ile	Glu	Asp	Cys	Pro	Ile	Asn	Asn	Pro	Arg	Ser	Gly	2660	2665	2670	
Arg	Ser	Pro	Thr	Gly	Asn	Thr	Pro	Pro	Val	Ile	Asp	Ser	Val	Ser	Glu	2675	2680	2685	
Lys	Ala	Asn	Pro	Asn	Ile	Lys	Asp	Ser	Lys	Asp	Asn	Gln	Ala	Lys	Gln	2690	2695	2700	
Asn	Val	Gly	Asn	Gly	Ser	Val	Pro	Met	Arg	Thr	Val	Gly	Leu	Glu	Asn	2705	2710	2715	2720
Arg	Leu	Asn	Ser	Phe	Ile	Gln	Val	Asp	Ala	Pro	Asp	Gln	Lys	Gly	Thr	2725	2730	2735	
Glu	Ile	Lys	Pro	Gly	Gln	Asn	Asn	Pro	Val	Pro	Val	Ser	Glu	Thr	Asn	2740	2745	2750	
Glu	Ser	Ser	Ile	Val	Glu	Arg	Thr	Pro	Phe	Ser	Ser	Ser	Ser	Ser	Ser	2755	2760	2765	
Lys	His	Ser	Ser	Pro	Ser	Gly	Thr	Val	Ala	Ala	Arg	Val	Thr	Pro	Phe	2770	2775	2780	
Asn	Tyr	Asn	Pro	Ser	Pro	Arg	Lys	Ser	Ser	Ala	Asp	Ser	Thr	Ser	Ala	2785	2790	2795	2800
Arg	Pro	Ser	Gln	Ile	Pro	Thr	Pro	Val	Asn	Asn	Asn	Thr	Lys	Lys	Arg	2805	2810	2815	
Asp	Ser	Lys	Thr	Asp	Ser	Thr	Glu	Ser	Ser	Gly	Thr	Gln	Ser	Pro	Lys	2820	2825	2830	

Arg His Ser Gly Ser Tyr Leu Val Thr Ser Val  
2835 2840

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 65 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CGGAATTCNN NNNNNNNAAC AGCNNNNNNN NNAATGAANN NCAAGTCTG NNNTGAGGAT 60  
CCTCA 65

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 65 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGGAATTCGA CTCAGAANNN NNNAACTTCA GANNNNNNAT CNNNNNNNNN GTCTGAGGAT 60  
CCTCA 65

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 65 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGGAATTCNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNTGAGGAT 60  
CCTCA 65